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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/528,673	03/23/2005	Tatsuo Hoshino	K21409USWO C038435/018565	2412
7590	06/16/2006		EXAMINER RAGHU, GANAPATHIRAM	
Stephen M Haracz Bryan Cave 1290 Avenue of the Americas New York, NY 10104			ART UNIT 1652	PAPER NUMBER

DATE MAILED: 06/16/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

DETAILED ACTION

Claims 1-18 are pending in this application.

Election/Restrictions

Restriction is required under 35 U.S.C. 121 and 372.

This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1.

In accordance with 37 CFR 1.499, applicant is required, in reply to this action, to elect a single invention to which the claims must be restricted.

Group I. Claims 1, 2, 5-8, 13, 16, drawn to a process for the production of L-ascorbic acid comprising: contacting an enzyme with a substrate selected from the group consisting of L-gulose, L-galactose, L-idose and L-talose or substrate is selected from the group consisting of L-gulono-1,4-lactone, L-gulonic acid, L-galactono-1,4-lactone, L-galctonic acid, L-idono-1,4-lactone, L-idonic acid, L-talono-1,4-lactone and L-talonic acid, wherein said enzyme has the amino acid sequence of SEQ ID NO: 2 .

Group II. Claims 3, 9, 11, 14, 17, drawn to a process for the production of L-gulono-1,4-lactone or L-gulonic acid from L-gulose, wherein said enzyme has the amino acid sequence of SEQ ID NO: 2, Enzyme B of *G. oxydans* DSM 4025.

Art Unit: 1652

Group III. Claims 4, 10, 12, 15, 18, drawn to a process for the production of L-galactono-1,4-lactone or L-galctonic acid from L-galactose, wherein said enzyme has the amino acid sequence of SEQ ID NO: 2, Enzyme B of *G. oxydans* DSM 4025.

The inventions listed as Groups I-III do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

The special technical features linking the inventions of Group I-III appears to be that they all relate to a process of production of L-ascorbic acid or L-gulono-1,4-lactone or L-gulonic acid by contacting with an enzyme, wherein said enzyme has the amino acid sequence of SEQ ID NO: 2 or a process of production of L-ascorbic acid or L-gulono-1,4-lactone or L-gulonic acid by contacting with an enzyme, wherein said enzyme is Enzyme B of *G. oxydans* DSM 4025.

However, Asakura et al., (1998, see sequence alignment provided) disclose the amino acid sequence of an enzyme from *G. oxydans* with alcohol and/or aldehyde dehydrogenase activity and L-gulonic acid is a known substrate for this enzyme, said enzyme has 100% sequence homology to SEQ ID NO: 2 of the instant application and therefore said enzyme can be used in the process for the production of L-gulonic acid or L-ascorbic acid.

Therefore the special technical feature linking the inventions of Group I-III does not constitute a special technical feature as defined by PCT Rule 13.2, as it does not define a contribution over the prior art.

Accordingly, Groups I-III are not so linked by the same or a corresponding special technical feature as to form a single inventive concept.

Art Unit: 1652

Applicant is advised that the reply to this requirement to be complete must include an election of the invention to be examined even though the requirement be traversed (37 CFR 1.143).


Applicant is reminded that upon the cancellation of claims to a non-elected invention, the inventorship must be amended in compliance with 37 CFR 1.48(b) if one or more of the currently named inventors is no longer an inventor of at least one claim remaining in the application. Any amendment of inventorship must be accompanied by a request under 37 CFR 1.48(b) and by the fee required under 37 CFR 1.17(i).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Ganapathirama Raghu whose telephone number is 571-272-4533. The examiner can normally be reached on 8 am - 4.30 pm. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ponnathapu Achutamurthy can be reached on 571-272-0928. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300 for regular communications and for After Final communications. Any inquiry of a general nature or relating to the status of the application or proceeding should be directed to the receptionist whose telephone number is 571-272-1600.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Ganapathirama Raghu, Ph.D.
Patent Examiner
Art Unit 1652

June 01, 2006.


REBECCA E. PROUTY
PRIMARY EXAMINER
GROUP 1800
1605

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 27, 2006, 12:51:34 ; Search time 197 Seconds
(without alignments)
1343.799 Million cell updates/sec

Title: US-10-528-673-2

Perfect score: 3069

Sequence: 1 MNPTLLRTSAVLLLTAPA.....AAIDSTSVGNAYVFPALPQ 579

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_8.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*
- 10: Geneseqp2006s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3069	100.0	579	2 AAW37876	AAW37876 Alcohol a
2	3069	100.0	579	8 ADN10956	Adn10956 Gluconoba
3	2765	90.1	580	8 ADI34121	Adi34121 Ketogulon
4	2611	85.1	579	2 AAW37873	AAW37873 Alcohol a
5	2590.5	84.4	612	8 ADW39238	Adw39238 P sacchar
6	2569.5	83.7	578	8 ADI34118	Adi34118 Ketogulon
7	2559.5	83.4	579	8 ADI34120	Adi34120 Ketogulon
8	2526.5	82.3	579	2 AAW37874	AAW37874 Alcohol a
9	2497	81.4	578	2 AAW37875	AAW37875 Alcohol a
10	1673	54.5	608	7 ADE94131	Ade94131 Alcohol/a
11	755.5	24.6	717	8 ADS21807	AdS21807 Bacterial
12	624.5	20.3	567	8 ADN24711	Adn24711 Bacterial
13	622	20.3	577	8 ADS43309	AdS43309 Bacterial
14	620	20.2	692	8 ADS42094	AdS42094 Bacterial
15	619	20.2	559	8 ADN21954	Adn21954 Bacterial
16	585	19.1	754	3 AAB35987	Aab35987 Sorbitol
17	578	18.8	623	8 ADN25393	Adn25393 Bacterial
18	554.5	18.1	601	8 ADN22277	Adn22277 Bacterial
19	552	18.0	685	7 ABO83287	Abo83287 Pseudomon
20	551.5	18.0	738	2 AAR20192	Aar20192 ADH compl
21	550.5	17.9	738	2 AAR13993	Aar13993 A.altoacet
22	547	17.8	592	8 ADN25035	Adn25035 Bacterial
23	529.5	17.3	532	8 ADN25034	Adn25034 Bacterial

24	524.5	17.1	706	8	ADS21805	AdS21805 Bacterial
25	513.5	16.7	683	8	ADN22276	Adn22276 Bacterial
26	490.5	16.0	742	2	AAR05235	Aar05235 Amino aci
27	482.5	15.7	592	8	ADS26936	AdS26936 Bacterial
28	482.5	15.7	592	8	ADS27298	AdS27298 Bacterial
29	482.5	15.7	593	8	ADS26560	AdS26560 Bacterial
30	416	13.6	792	8	ADN24984	Adn24984 Bacterial
31	416	13.6	792	8	ADN22225	Adn22225 Bacterial
32	412	13.4	803	7	ADD24941	Add24941 Escherich
33	412	13.4	823	8	ADU40628	Adu40628 Membrane-
34	411	13.4	743	6	ABR42659	ABr42659 Gluconic
35	411	13.4	743	9	AED03436	Aed03436 S-keto-D-
36	408	13.3	804	8	ADN22168	Adn22168 Bacterial
37	408	13.3	804	8	ADN24927	Adn24927 Bacterial
38	407	13.3	798	8	ADS26380	AdS26380 Bacterial
39	407	13.3	798	8	ADS27130	AdS27130 Bacterial
40	407	13.3	798	8	ADS26748	AdS26748 Bacterial
41	399	13.0	796	8	ADN18050	Adn18050 Bacterial
42	399	13.0	796	8	ADT87278	Adt87278 E.coli 8c
43	396.5	12.9	788	9	ADY26616	Ady26616 Amino aci
44	396.5	12.9	788	9	ADY26591	Ady26591 Amino aci
45	396.5	12.9	788	9	ADX44826	Adx44826 G. oxydan

ALIGNMENTS

RESULT 1

AAW37876
ID AAW37876 standard; protein, 579 AA.

XX
AC AAW37876;

DT 10-AUG-1998 (first entry)

XX
DE Alcohol and/or aldehyde dehydrogenase B amino acid sequence.

XX
KW Alcohol/aldehyde dehydrogenase B enzyme; recombinant organism; aldehyde, ketone, carboxylic acid; L-sorbose; D-sorbitol; 2-keto-L-gulononic acid, L-ascorbic; inhibition.

XX
OS Gluconobacter oxydans.

XX
FH Key Location/Qualifiers

FT Peptide 1..23 /note= "signal peptide"

FT Protein 24..579 /note= "mature protein"

XX
EP832974-A2.

XX
PD 01-APR-1998.

XX
PF 11-SEP-1997; 97EP-00115801.

XX
PR 19-SEP-1996; 96EP-00115001.

XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG P.

XX
PI Asakura A, Hoshino T, Ojima S, Shinjoh M, Tomiyama N;

XX
DR WPI; 1998-1955228/18.

XX
N-PSDB; AAV29054.

XX
PT Recombinant Gluconobacter oxydans alcohol and/or aldehyde dehydrogenase enzyme(s) - useful for converting substrate(s), e.g. L-sorbose or D-sorbitol to 2-keto-L-gulononic acid.

XX
PS Claim 1; Page 44-46; 59pp; English.

XX
CC This is the amino acid sequence for the Gluconobacter oxydans alcohol and/or aldehyde dehydrogenase B enzyme. The enzymes or recombinant organisms can be used to convert suitable substrates to aldehydes,

CC ketones or carboxylic acids, especially to convert L-sorbose or D-
 CC sorbitol to 2-keto-L-gulononic acid, which can be converted to L-ascorbic
 CC acid by standard procedures. The derivatives of ADH enzymes have desired
 CC substrate specificity, higher affinity to a substrate, lower affinity to
 CC an inhibitory compound, higher stability against temperature and/or pH
 CC and higher catalytic speed
 XX
 SQ Sequence 579 AA;

Query Match 100.0%; Score 3069; DB 2; Length 579;
 Best Local Similarity 100.0%; Pred. No. 5.5e-244;
 Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNPTLLRTSAVLLTAPAAFAQVPTITDELLANPAGEWINGRQENRHSPLTQIT 60
 DB 1 MNPTLLRTSAVLLTAPAAFAQVPTITDELLANPAGEWINGRQENRHSPLTQIT 60
 QY 61 ADVNGQLQVWARGMEAGAVQVTPMIDHGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA 120
 DB 61 ADVNGQLQVWARGMEAGAVQVTPMIDHGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA 120
 QY 121 VATLNAQDQDRKRGVALYGTSLYFSSWDNHLIALDMETGVVDFVVERGSGDGLTSNTTGP 180
 DB 121 VATLNAQDQDRKRGVALYGTSLYFSSWDNHLIALDMETGVVDFVVERGSGDGLTSNTTGP 180
 QY 181 IVANGVIVAGSTCOYSPYGCPIFGHDSATGBELWRNHFIPQEGSGDGTWGNDFEARWMT 240
 DB 181 IVANGVIVAGSTCOYSPYGCPIFGHDSATGBELWRNHFIPQEGSGDGTWGNDFEARWMT 240
 QY 241 GWNGQITVPTNLVYFGTGVGPASSETQRTGCTGTYGNTNTPAVRPTDGEIWRHQTLP 300
 DB 241 GWNGQITVPTNLVYFGTGVGPASSETQRTGCTGTYGNTNTPAVRPTDGEIWRHQTLP 300
 QY 301 PRDNWDQECTFEMVAVNDVQPSAEMGLRAINFNAATGERRVLTGAPCKTGTWMSFDAA 360
 DB 301 PRDNWDQECTFEMVAVNDVQPSAEMGLRAINFNAATGERRVLTGAPCKTGTWMSFDAA 360
 QY 361 SGEFLWARDNTYTNMIASIDETGLVTNVEDAVLKELDVEYDVCPTFLGGRDWSSAALNPD 420
 DB 361 SGEFLWARDNTYTNMIASIDETGLVTNVEDAVLKELDVEYDVCPTFLGGRDWSSAALNPD 420
 QY 421 TGIYFLPLNACVDINAVDQEPFSAIDVNTSATAKLAPGFENMGRIIDAIDISTGRTLWSA 480
 DB 421 TGIYFLPLNACVDINAVDQEPFSAIDVNTSATAKLAPGFENMGRIIDAIDISTGRTLWSA 480
 QY 481 ERPAANYSPLVSTAGGVNGGTDYFRALQSQTGTSLWQARLATVATGQALSYELDGVQ 540
 DB 481 ERPAANYSPLVSTAGGVNGGTDYFRALQSQTGTSLWQARLATVATGQALSYELDGVQ 540
 QY 541 YIAIGAGGLTYGTQLNAPLAEAIDSTS VGNAIYVPALPQ 579
 DB 541 YIAIGAGGLTYGTQLNAPLAEAIDSTS VGNAIYVPALPQ 579

RESULT 2

ID ADN10956
 ADN10956 standard; protein; 579 AA.

AC ADN10956;

DT 01-JUN-2004 (first entry)

DE Gluconobacter oxydans Enzyme B, used in ascorbic acid production.

KW Enzyme B; ascorbic acid; vitamin C; L-gulonono-1,4-lactone; L-gulononic acid;
 KW L-galactono-1,4-lactone; L-galactonic acid.

OS Gluconobacter oxydans.

PN WO2004029267-A1.

PD 08-APR-2004.

XX

PP 22-SEP-2003; 2003WO-EP010489.

XX 27-SEP-2002; 2002BP-00021602.

XX (STAM) DSM IP ASSETS BV.

XX Hoshino T, Shinjoh M;

XX WPI/ 2004-329889/30.

DR N-PSOB; ADN10955.

XX Producing L-ascorbic acid using enzyme B of Gluconobacter oxydans, from
 PT substrates L-gulose, L-galactose, L-idose, and L-talose.

XX Claim 1, SEQ ID NO 2; 24pp; English.

XX The present sequence is the protein sequence of Enzyme B from
 CC Gluconobacter oxydans strain DSM 4025. Enzyme B has a molecular weight of
 CC about 60,000 Da by SDS-PAGE, substrate specificity for primary and
 CC secondary alcohols and aldehydes, is stable in the pH range 6-9 with
 CC optimal activity at about pH 8.0, and is inhibited by Cu²⁺, Zn²⁺, Mn²⁺,
 CC Fe²⁺ and Fe³⁺. The present invention provides the use of this enzyme in a
 CC process for producing L-ascorbic acid from L-gulose, L-galactose, L-idose
 CC or L-talose, or from L-gulonono-1,4-lactone, L-gulonic acid, L-galactono-
 CC 1,4-lactone, L-galactonic acid, L-idono-1,4-lactone, L-idonic acid, L-
 CC talono-1,4-lactone and L-talonic acid. Enzyme B is also used in a process
 CC for the production of L-gulonono-1,4-lactone or L-gulonic acid from L-
 CC gulose, and L-galactono-1,4-lactone or L-galactonic acid from L-
 CC galactose. The processes involve contacting the enzyme with the
 CC respective substrate and isolating the product from the reaction mixture.
 CC The process is conducted for 1-20 hours at pH 1-9 (preferably pH 2-8) and
 CC 13-45 (preferably 18-42) degrees C. Production of L-gulonono-1,4-lactone/L-
 CC gulonic acid from L-gulose, vitamin C from L-gulonono-1,4-lactone/L-
 CC gulonic acid, L-galactono-1,4-lactone/L-galactonic acid from L-galactose, and
 CC vitamin C from L-galactono-1,4-lactone/L-galactonic acid by recombinant
 CC Escherichia coli JM109 carrying the Enzyme B gene is described in
 CC examples from the invention.

XX Sequence 579 AA;

QY Query Match 100.0%; Score 3069; DB 8; Length 579;
 DB Best Local Similarity 100.0%; Pred. No. 5.5e-244;
 Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNPTLLRTSAVLLTAPAAFAQVPTITDELLANPAGEWINGRQENRHSPLTQIT 60

DB 1 MNPTLLRTSAVLLTAPAAFAQVPTITDELLANPAGEWINGRQENRHSPLTQIT 60

QY 61 ADVNGQLQVWARGMEAGAVQVTPMIDHGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA 120

DB 61 ADVNGQLQVWARGMEAGAVQVTPMIDHGVMYLANPGDVIQALDAQTGDLIWEHRRQLPA 120

QY 121 VATLNAQDQDRKRGVALYGTSLYFSSWDNHLIALDMETGVVDFVVERGSGDGLTSNTTGP 180

DB 121 VATLNAQDQDRKRGVALYGTSLYFSSWDNHLIALDMETGVVDFVVERGSGDGLTSNTTGP 180

QY 181 IVANGVIVAGSTCOYSPYGCPIFGHDSATGBELWRNHFIPQEGSGDGTWGNDFEARWMT 240

DB 181 IVANGVIVAGSTCOYSPYGCPIFGHDSATGBELWRNHFIPQEGSGDGTWGNDFEARWMT 240

QY 241 GWNGQITVPTNLVYFGTGVGPASSETQRTGCTGTYGNTNTPAVRPTDGEIWRHQTLP 300

DB 241 GWNGQITVPTNLVYFGTGVGPASSETQRTGCTGTYGNTNTPAVRPTDGEIWRHQTLP 300

QY 301 PRDNWDQECTFEMVAVNDVQPSAEMGLRAINFNAATGERRVLTGAPCKTGTWMSFDAA 360

DB 301 PRDNWDQECTFEMVAVNDVQPSAEMGLRAINFNAATGERRVLTGAPCKTGTWMSFDAA 360

QY 361 SGEFLWARDNTYTNMIASIDETGLVTNVEDAVLKELDVEYDVCPTFLGGRDWSSAALNPD 420

DB 361 SGEFLWARDNTYTNMIASIDETGLVTNVEDAVLKELDVEYDVCPTFLGGRDWSSAALNPD 420

QY 421 TGIYFLPLNACVDINAVDQEPFSAIDVNTSATAKLAPGFENMGRIIDAIDISTGRTLWSA 480

DB 421 TGIYFLPLNACVDINAVDQEPFSAIDVNTSATAKLAPGFENMGRIIDAIDISTGRTLWSA 480